Package 'ShapeRotator'

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Type Package

Title Standardised Rigid Rotations of Articulated Three-Dimensional
Structures

Version 0.1.0

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Description Here we describe a simple geometric rigid rotation approach that removes the effect of random translation and rotation, enabling the morphological analysis of 3D articulated structures. Our method is based on Cartesian coordinates in 3D space so it can be applied to any morphometric problem that also uses 3D coordinates. See Vidal-García, M., Bandara, L., Keogh, J.S. (2018) <doi:10.1002/ece3.4018>.

License GPL (>= 2)

RoxygenNote 7.1.0

NeedsCompilation no

Encoding UTF-8

Repository CRAN

Imports plot3D

Suggests geomorph

URL https://github.com/marta-vidalgarcia/ShapeRotator

BugReports https://github.com/marta-vidalgarcia/ShapeRotator/issues

LazyData true

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R topics documented:

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double.rotation	*double.rotation*

Description

Rotates two arrays in a two-points articulation (e.g. skull and mandible)

Usage

```
double.rotation(data.1, data.2, land.a, land.b, land.c, land.d,
  land.e, land.f, land.g, land.h, angle)
```

Arguments

data.1	an object of the class "array" that contains translated three-dimensional landmarks for structure #1
data.2	an object of the class "array" that contains translated three-dimensional landmarks for structure #2
land.a	an integer object that indicates the position of the three-dimensional landmark A
land.b	an integer object that indicates the position of the three-dimensional landmark B
land.c	an integer object that indicates the position of the three-dimensional landmark C
land.d	an integer object that indicates the position of the three-dimensional landmark D
land.e	an integer object that indicates the position of the three-dimensional landmark E
land.f	an integer object that indicates the position of the three-dimensional landmark F
land.g	an integer object that indicates the position of the three-dimensional landmark G
land.h	an integer object that indicates the position of the three-dimensional landmark H
angle	an object of the class "numeric" that contains the rotation angle in degrees (from 0° to 360°)

Details

This function allows the rigid rotation of two structures from a two-points articulation (e.g. skull and mandible). It allows to select the desired angle between the two structures so that we can perform the rigid rotation of each structure positioning them in the selected angle in relation to each other, by providing the desired angle in degrees (from 0 to 360 degrees). Even though each of these rotations are calculated internally (only the four landmarks per structure and the desired angle between them need to be provided), it will be beneficial to choose landmarks that are spatially arranged in a way that facilitates the rotation process, and results in the rotating multi-structure being placed in a biologically-relevant angle between each sub-structure. ShapeRotator will give a warning message if the landmarks chosen are not optimal (i.e. the position and orientation of the two structures vary across the specimens due to morphological variability and not because of the rigid rotation).

Value

Returns a list of two object where $rotated1 gives the first rotated array and $rotated2 gives the second

Author(s)

Marta Vidal-Garcia

References

M. Vidal-García, L. Bandara and J.S. Keogh. 2018. ShapeRotator: An R tool for standardized rigid rotations of articulated three-dimensional structures with application for geometric morphometrics. Ecology and Evolution. DOI: 10.1002/ece3.4018

Examples

```
#Data
data(double_data_1)
data(double_data_2)
data.1 <- double_data_1
data.2 <- double_data_2

#Landmarks
land.a=55
land.b=49
land.c=54
land.d =4
land.e=22
land.f=21
land.g=2
land.h=11

# We can rigidly rotate each structure relative to each other in multiple
# angles (e.g. 0, 15, 45, 90, or 120 degrees)
rotation_0 = double.rotation(data.1, data.2, land.a, land.b, land.c, land.d,
land.e, land.f, land.g, land.h, 0)
rotation_15 = double.rotation(data.1, data.2, land.a, land.b, land.c, land.d,
```

```
land.e, land.f, land.g, land.h, 15)
rotation_45 = double.rotation(data.1, data.2, land.a, land.b, land.c, land.d,
land.e, land.f, land.g, land.h, 45)
rotation_90 = double.rotation(data.1, data.2, land.a, land.b, land.c, land.d,
land.e, land.f, land.g, land.h, 90)
rotation_120 = double.rotation(data.1, data.2, land.a, land.b, land.c,
land.d, land.e, land.f, land.g, land.h, 120)

# The function returns a list of two objects that correspond to each rotated
# structure
rotation_0$rotated1 #rotated dataset 1 #(e.g. skull)
rotation_0$rotated2 #rotated dataset 2 #(e.g. mandible)

# The two datasets can be joined with the function join.arrays()
head_0degrees <- join.arrays(rotation_0$rotated1, rotation_0$rotated2)
```

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double_data_1 *Landmark data from head-first burrowing worm lizards' crania*

Description

Landmark data from head-first burrowing worm lizards' crania (Kazi & Hipsley, 2018)

Usage

```
data(double_data_1)
```

Format

An array with landmark data (crania)

References

S. Kazi & C.A. Hipsley. 2018. Conserved evolution of skull shape in Caribbean head-first burrowing worm lizards (Squamata: Amphisbaenia) Biological Journal of the Linnean Society 125:14-29

M. Vidal-García, L. Bandara and J.S. Keogh. 2018. ShapeRotator: An R tool for standardized rigid rotations of articulated three-dimensional structures with application for geometric morphometrics. Ecology and Evolution. DOI: 10.1002/ece3.4018

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double_data_2 *Landmark data from head-first burrowing worm lizards' mandibles*

Description

Landmark data from head-first burrowing worm lizards' mandibles (Kazi & Hipsley, 2018)

Usage

```
data(double_data_2)
```

Format

An array with landmark data (mandibles)

References

S. Kazi & C.A. Hipsley. 2018. Conserved evolution of skull shape in Caribbean head-first burrowing worm lizards (Squamata: Amphisbaenia) Biological Journal of the Linnean Society 125:14-29

M. Vidal-García, L. Bandara and J.S. Keogh. 2018. ShapeRotator: An R tool for standardized rigid rotations of articulated three-dimensional structures with application for geometric morphometrics. Ecology and Evolution. DOI: 10.1002/ece3.4018

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join.arrays *join.arrays*

Description

Joins the two rotated arrays and returns a single array

Usage

```
join.arrays(data.1, data.2)
```

Arguments

data.1	an object of the class "array" that contains the rotated three-dimensional landmarks for structure #1 (e.g. skull)
data.2	an object of the class "array" that contains the rotated three-dimensional landmarks for structure #2 (e.g. mandible)

Details

This function join the two arrays that were rotated using double.rotation() or simple.rotation() and return a big array from joining the two smaller arrays. It is possible to translate one of the objects after the rotation, in the case of not wanting them in contact to one another, or in a slightly different location. The vector used in the translation might have to change depending on the angle used in the rotation function, in order to represent biologically-relevant positions of the two structures relative to one another.

Value

This function returns an array of the joined two arrays comprising the two rotated structures (e.g. mandible and skull).

Author(s)

Marta Vidal-Garcia

References

M. Vidal-García, L. Bandara and J.S. Keogh. 2018. ShapeRotator: An R tool for standardized rigid rotations of articulated three-dimensional structures with application for geometric morphometrics. Ecology and Evolution. DOI: 10.1002/ece3.4018

Examples

```
rotation_45 = double.rotation(data.1, data.2, land.a, land.b, land.c, land.d,
land.e, land.f, land.g, land.h, 45)

rotation_45_t <- join.arrays(rotation_45$rotated1, rotation_45$rotated2)

# The datasets can also be joined after further translation
rotation_45_t <- join.arrays(rotation_45$rotated1,
translate(rotation_45$rotated2, land.e , skull_translate))
```

---

  match.datasets   *match.datasets*

Description

Matches two arrays by their dimnames

Usage

```
match.datasets(data.1, data.2)
```

Arguments

data.1   an object of the class "array" that contains three-dimensional landmarks for structure #1 (e.g. skull)

data.2   an object of the class "array" that contains three-dimensional landmarks for structure #2 (e.g. mandible)

Details

Takes the two translated arrays and joined them by dimnames. Unmatched datasets (specimens missing in data.1 or data.2) are deleted.

Value

This function returns a list with the two translated arrays of dimensions (p, 3, n), in which dimnames associated with each specimen (n) are in the same order.

Author(s)

Marta Vidal-Garcia

References

M. Vidal-García, L. Bandara and J.S. Keogh. 2018. ShapeRotator: An R tool for standardized rigid rotations of articulated three-dimensional structures with application for geometric morphometrics. Ecology and Evolution. DOI: 10.1002/ece3.4018

Examples

```
# We need to match the dimnames of the translated datasets, but we have two
# extra specimens in data.1_t

length(dimnames(data.1_t)[[3]]) # n=12
length(dimnames(data.2_t)[[3]])  # n=10
matched <- match.datasets(data.1_t, data.2_t)

# When we matched the arrays, only matrices from specimens present in both
# datasets will be kept

length(dimnames(matched$matched1)[[3]]) # n=10

length(dimnames(matched$matched2)[[3]])  # n=10
```

plot_rotation_3D	*plot_rotation_3D*

Description

Plots the two rotated datasets in 3D

Usage

```
plot_rotation_3D(joined.data, data.1, data.2, specimen.num)
```

Arguments

joined.data   an object of the class "array" that contains the joined rotated arrays (data.1three-dimensional landmarks for structure #1 (e.g. skull). It can either be the original dataset, the translated array, or the rotated array

data.1   an object of the class "array" that contains three-dimensional landmarks for structure #1 (e.g. skull). It can either be the original dataset, the translated array, or the rotated array

data.2   an object of the class "array" that contains three-dimensional landmarks for structure #2 (e.g. mandible). It can either be the original dataset, the translated array, or the rotated array

specimen.num   an integer object that indicates which specimen will be plotted. The number of the specimen to be plotted corresponds to the position in the "joined.data" array

Details

Plots the two rotated datasets in 3D for a specimen (specimen.num), and each structure is plotted with a different colour. Default is black and red. This uses the function scatter3D from the R package plot3D (https://cran.r-project.org/web/packages/plot3D/) internally.

Value

This function returns a 3D plot of the rotated structures (e.g. mandible and skull).

Author(s)

Marta Vidal-Garcia

References

M. Vidal-García, L. Bandara and J.S. Keogh. 2018. ShapeRotator: An R tool for standardized rigid rotations of articulated three-dimensional structures with application for geometric morphometrics. Ecology and Evolution. DOI: 10.1002/ece3.4018

Examples

```
rotation_45 = double.rotation(data.1, data.2, land.a, land.b, land.c, land.d,
land.e, land.f, land.g, land.h, 45)

rotation_45_t <- join.arrays(rotation_45$rotated1,
translate(rotation_45$rotated2, land.e , skull_translate))

plot_rotation_3D(rotation_45_t, data.1, data.2, specimen.num = 1)
```

---

simple.rotation   *simple.rotation*

Description

Rotates two arrays in a single-point articulation (e.g. two limb bones).

Usage

```
simple.rotation(data.1, data.2, land.a, land.b, land.c,
  land.d, land.e, land.f, angle)
```

Arguments

data.1	an object of the class "array" that contains translated three-dimensional landmarks for structure #1
data.2	an object of the class "array" that contains translated three-dimensional landmarks for structure #2
land.a	an integer object that indicates the position of the three-dimensional landmark A
land.b	an integer object that indicates the position of the three-dimensional landmark B
land.c	an integer object that indicates the position of the three-dimensional landmark C
land.d	an integer object that indicates the position of the three-dimensional landmark D
land.e	an integer object that indicates the position of the three-dimensional landmark E
land.f	an integer object that indicates the position of the three-dimensional landmark F
angle	an object of the class "numeric" that contains the rotation angle in degrees (from 0° to 360°)

Details

This function allows the rigid rotation of two structures from a single-point articulation (e.g. humerus and radioulna). It allows to select the desired angle between the two structures so that we can perform the rigid rotation of each structure positioning them in the selected angle in relation to each other, by providing the desired angle in degrees (from 0° to 360°). Even though each of these rotations are calculated internally (only the three landmarks per structure and the desired angle between them need to be provided), it will be beneficial to choose landmarks that are spatially arranged in a way that facilitates the rotation process, and results in the rotating multi-structure being placed in a biologically-relevant angle between each sub-structure. ShapeRotator will give a warning message if the landmarks chosen are not optimal (i.e. the position and orientation of the two structures vary across the specimens due to morphological variability and not because of the rigid rotation).

Value

This function returns a translated T array of dimensions (p, 3, n), in which p indicates the number of landmarks, and n the number of specimens included in the array. The translated array will keep the dimnames associated with each specimen (n).

Author(s)

Marta Vidal-Garcia

References

M. Vidal-García, L. Bandara and J.S. Keogh. 2018. ShapeRotator: An R tool for standardized rigid rotations of articulated three-dimensional structures with application for geometric morphometrics. Ecology and Evolution. DOI: 10.1002/ece3.4018

Examples

```
#Data
data.1 <- simple_data_1
data.2 <- simple_data_2

#Landmarks
land.a=55
land.b=49
land.c=54

land.d =4
land.e=22
land.f=21

# We can rigidly rotate each structure relative to each other in multiple
# angles (e.g. 0, 15, 45, 90, or 120 degrees)
rotation_0 = simple.rotation(data.1, data.2, land.a, land.b, land.c,
land.d, land.e, land.f, 0)

rotation_15 = simple.rotation(data.1, data.2, land.a, land.b, land.c,
land.d, land.e, land.f, 15)
```

```
rotation_45 = simple.rotation(data.1, data.2, land.a, land.b, land.c,
land.d, land.e, land.f, 45)

rotation_90 = simple.rotation(data.1, data.2, land.a, land.b, land.c,
land.d, land.e, land.f, 90)

rotation_120 = simple.rotation(data.1, data.2, land.a, land.b, land.c,
land.d, land.e, land.f, 120)

# The function returns a list of two objects that correspond to each rotated
# structure
rotation_0$rotated1 #rotated dataset 1 #(e.g. radioulna)
rotation_0$rotated2 #rotated dataset 2 #(e.g. humerus)

# The two datasets can be joined with the function join.arrays()
arm_0degrees <- join.arrays(rotation_0$rotated1, rotation_0$rotated2)
```

---

simple_data_1   *Landmark data from frog humerus*

Description

Landmark data from frog humerus (Vidal-Garciía & Keogh, 2017)

Usage

```
data(simple_data_1)
```

Format

An array with landmark data (humerus)

References

M. Vidal-García & J.S. Keogh. 2017. Phylogenetic conservatism in skulls and evolutionary lability in limbs–morphological evolution across an ancient frog radiation is shaped by diet, locomotion and burrowing. BMC evolutionary biology 17:165

M. Vidal-García, L. Bandara and J.S. Keogh. 2018. ShapeRotator: An R tool for standardized rigid rotations of articulated three-dimensional structures with application for geometric morphometrics. Ecology and Evolution. DOI: 10.1002/ece3.4018

---

simple_data_2   *Landmark data from frog radioulnas*

Description

Landmark data from frog radioulnas (Vidal-Garciía & Keogh, 2017)

Usage

```
data(simple_data_2)
```

Format

An array with landmark data (radioulnas)

References

M. Vidal-García & J.S. Keogh. 2017. Phylogenetic conservatism in skulls and evolutionary lability in limbs–morphological evolution across an ancient frog radiation is shaped by diet, locomotion and burrowing. BMC evolutionary biology 17:165

M. Vidal-García, L. Bandara and J.S. Keogh. 2018. ShapeRotator: An R tool for standardized rigid rotations of articulated three-dimensional structures with application for geometric morphometrics. Ecology and Evolution. DOI: 10.1002/ece3.4018

---

translate   *translate*

Description

Translates array T to origin point.

Usage

```
translate(T, landmark, origin = c(0,0,0))
```

Arguments

T	an object of the class "array" that contains three-dimensional landmarks for 'n' specimens
landmark	an integer object that indicates the position of the three-dimensional landmark that will be used to translate each matrix of landmarks to the point of origin.
origin	a vector that contains three-dimensional coordinates (x, y, z) indicating where the origin point should be translanted to.

Details

Takes an array T and an index in the array landmark, and translates it to the origin. Each structure will be translated to the point of origin so that p0 =(0,0,0). We will be translating landmark A from structure 1 and landmark D from structure 2 for a single-point articulated rotation. And landmark A from structure 1 and landmark E from structure 2 for a double rotation (double-point articulated rotation). Thus, the distance from the coordinates of landmark A (Ax, Ay, Az) is substracted from all the landmarks in all specimens. For example (Nx - Ax, Ny - Ay, Nz - Az) for landmark N, for structure 1. For structure 2, the distance from the coordinates of landmark D or E depending on the type of rotation. For example, in a double rotation, (Ex, Ey, Ez) is substracted from all the landmarks in all specimens: (Nx - Ex, Ny - Ey, Nz - Ez). Landmarks A and E will equal (0,0,0), so that Ax=Ay=Az=Ex=Ey=Ez=0. The default is to set the origin to (0,0,0), but this can be specified to be something else. In order to use this function, the landmark data needs to be imported to the R environment using geomorph (Adams et al., 2018)

Value

This function returns a translated T array of dimensions (p, 3, n), in which p indicates the number of landmarks, and n the number of specimens included in the array. The translated array will keep the dimnames associated with each specimen (n).

Author(s)

Marta Vidal-Garcia

References

Adams, D. C., M. L. Collyer, and A. Kaliontzopoulou. 2018. Geomorph: Software for geometric morphometric analysis. R package version 3.0.6. Available at http://CRAN.R-project.org/package=geomorph.

M. Vidal-García, L. Bandara and J.S. Keogh. 2018. ShapeRotator: An R tool for standardized rigid rotations of articulated three-dimensional structures with application for geometric morphometrics. Ecology and Evolution. DOI: 10.1002/ece3.4018

Examples

```
#Data
data(double_data_1)
data(double_data_2)
data.1 <- double_data_1
data.2 <- double_data_2

#Landmarks
land.a=55
land.b=49
land.c=54
land.d=4

land.e=22
land.f=21
land.g=2
land.h=11
```

```
# Translate the data
data.1_t <- translate(data.1, land.a)
data.2_t <- translate(data.2, land.e)
```

Index